

MAPK Targets Include Proteins Known or Predicted to Enter the Secretory Pathway

PGU1	secreted endopolygalacturonase
FLO11	GPI-linked cell surface adhesion factor
TOT10/YEL033W	novel
SRD1	Zinc finger protein
TOT12/YKR105C	putative permease
TOT13/YOR225W	putative membrane protein
FLO5	GPI-linked cell surface adhesion factor
DDR48	cell surface protein
TOT11/YLR042C	GPI-linked cell surface protein
TOT7/YER158C	Homolog of mating morphogenesis protein Afr1
TOT8/YIL117C	Homolog of Chitin Synthase III subunit
TOT20/YHL049C	telomeric protein family member
TOT15/YLR434C	novel
TOT14/YBR113W	putative membrane protein
TOT9/YIR013C	Zinc finger protein
PHO84	phosphate transporter, sugar permease family
KTR2	protein mannosyltransferase homolog
SJH1	Sac1-related inositol phosphate 5-phosphatase homolog





Sytematic Knockout Experiments

GENE	Haploid Invasion	Diploid Filamentation
<i>PGU1</i>	+++	+++
<i>FLO11</i>	-	-
<i>TOT10/YEL033W</i>	+	+
<i>SRD1</i>	ND	ND
<i>TOT12/YKR105C</i>	+++	+++
<i>TOT13/YOR225W</i>	+++	+++
<i>FLO5</i>	+++	+++
<i>DDR48</i>	+++	+++
<i>TOT11/YLR042C</i>	+++	+++
<i>TOT7/YER158C</i>	+++	+++
<i>TOT8/YIL117C</i>	+++	+++
<i>TOT20/YHL049C</i>	ND	ND
<i>TOT15YLR434C</i>	+++	+++
<i>TOT14/YBR113W</i>	+++	+++
<i>TOT9/YIR013C</i>	+++	+++
<i>PHO84</i>	+++	+++
<i>KTR2</i>	+++	+++
<i>SJH1</i>	+++	+++

Gene Induction by the Plant-Specific Carbohydrate Polygalacturonic Acid and Its Hydrolysis Product

Genes Selectively Induced by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>XBP1</i>	2.40	6.65	Stress-induced transcriptional repressor
<i>YHR217C</i> (—f)	1.30	6.00	Protein of unknown function
<i>YPL080C</i>	2.80	5.70	Protein of unknown function
<i>YPR098C</i>	1.16	5.49	Protein of unknown function
<i>YHL040C</i>	2.04	5.00	Putative MFS Permease
<i>YOL080C</i>	1.35	4.74	Protein with similarity to Rnh70p and Pan2p
<i>PHO84</i>	1.39	4.70	phosphate transport, sugar permease homolog*
<i>YMR293C</i>	1.29	4.07	Protein with similarity to amidase
<i>YLR184W</i>	1.33	3.24	Protein of unknown function
<i>YIL011W</i>	1.01	3.01	Protein with similarity to PAU1 family
<i>CYT1</i>	1.02	2.82	Cytochrome c1
<i>ATP11</i>	1.29	2.65	F1-ATP synthase assembly protein
<i>YOR091W</i>	1.17	2.51	Protein of unknown function
<i>PAU3</i>	1.02	2.46	Stress-induced protein of the PAU1 family
<i>SKO1</i>	0.47	2.35	ATF/CREB transcriptional repressor
<i>MSI4</i>	0.73	2.06	Rab guanine nucleotide dissociation inhibitor
Regulated by Filamentation MAPK Pathway*			

Genes Selectively Induced by Galacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>VPS1</i>	4.03	1.69	Vacuolar sorting protein, dynamin GTPase

Gene Repression by the Plant-Specific Carbohydrate Polygalacturonic Acid and its Hydrolysis Product

Genes Selectively Repressed by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
COP1/SEC33	0.63	0.17	alpha subunit of coatamer complex
YOL002C	1.36	0.18	Protein of unknown function
YDL173W	0.96	0.24	Protein of unknown function
COQ2	1.37	0.25	coenzyme Q (ubiquinone) biosynthesis
YIL176C (f)	0.86	0.30	Protein with similarity to PAU1 family
YFL032W	0.80	0.30	Protein of unknown function
RPS33A	1.10	0.34	Ribosomal protein S28A
ARC35	1.25	0.39	Component of ARP2/3 complex
RPS26A	0.87	0.39	Ribosomal protein S26A
RPS10A	1.02	0.46	Ribosomal protein S10A

Genes Selectively Repressed by Galacturonic Acid

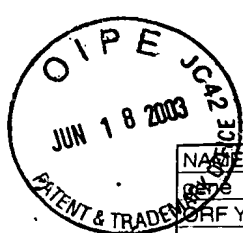
gene	GA/-	PGA/-	Protein Information
YEL033W	0.12	0.38	Protein of unknown function*
VID24	0.24	1.46	Vacuolar import and degradation of Fbp1
NDC1	0.29	1.02	Spindle pole body duplication factor
SKO1	0.47	2.35	ATF/CREB transcriptional repressor

*Regulated by the Filamentation MAPK Pathway



WT	1001	1012	1017	TECHC	STET14	VPO Data Log
282	47	173	173	747	2020	Self-healing function.
50	20	34	21	209	38	1. Multi-layered, flexible, and durable.
178	20	41	30	255	30	1. Self-healing function.
492	147	147	147	147	660	1. Self-healing function.
91	33	20	20	275	980	1. Self-healing function.
57	20	20	20	350	1250	1. Self-healing function.
657	90	195	336	657	1250	1. Self-healing function.
261	59	60	75	503	1250	1. Self-healing function.
112	20	44	45	116	1250	1. Self-healing function.
105	21	31	28	133	1250	1. Self-healing function.
75	30	48	138	389	237	1. Self-healing function.
672	134	364	685	655	237	1. Self-healing function.
89	28	20	20	120	237	1. Self-healing function.
78	25	78	28	113	237	1. Self-healing function.
724	160	316	620	232	237	1. Self-healing function.
68	30	68	78	128	237	1. Self-healing function.
612	33	40	40	120	237	1. Self-healing function.
170	28	20	108	104	237	1. Self-healing function.
132	65	118	162	233	237	1. Self-healing function.
20	20	20	20	89	237	1. Self-healing function.
305	137	167	162	472	237	1. Self-healing function.
59	34	87	95	117	237	1. Self-healing function.
401	126	327	304	424	237	1. Self-healing function.
20	26	36	47	87	237	1. Self-healing function.
57	33	75	73	110	237	1. Self-healing function.
97	35	20	27	113	237	1. Self-healing function.
88	20	74	69	93	237	1. Self-healing function.
48	20	105	101	83	237	1. Self-healing function.
44	21	42	94	127	237	1. Self-healing function.
153	57	133	173	144	237	1. Self-healing function.
20	20	20	20	92	237	1. Self-healing function.
178	30	116	116	200	237	1. Self-healing function.
102	655	697	731	131	237	1. Self-healing function.
153	44	54	40	118	237	1. Self-healing function.
104	39	137	133	98	237	1. Self-healing function.
149	76	176	186	181	237	1. Self-healing function.
87	86	80	121	92	237	1. Self-healing function.
209	87	217	135	197	237	1. Self-healing function.
47	47	176	170	195	237	1. Self-healing function.
255	106	176	125	238	237	1. Self-healing function.
232	1574	158	182	349	237	1. Self-healing function.
176	30	144	95	196	237	1. Self-healing function.
738	440	1418	1405	971	237	1. Self-healing function.
683	642	717	632	1776	237	1. Self-healing function.
238	200	429	230	415	237	1. Self-healing function.
1947	1004	2056	1789	2089	237	1. Self-healing function.
1555	820	1815	1324	1897	237	1. Self-healing function.
458	46	59	47	135	237	1. Self-healing function.
105	63	119	85	127	237	1. Self-healing function.
650	426	327	274	658	237	1. Self-healing function.
765	607	670	695	1218	237	1. Self-healing function.
185	174	253	148	349	237	1. Self-healing function.
60	20	114	91	40	237	1. Self-healing function.
127	63	85	115	126	237	1. Self-healing function.
67	38	77	122	76	237	1. Self-healing function.
75	45	146	109	90	237	1. Self-healing function.
53	41	124	131	82	237	1. Self-healing function.

Figure 7 Figures 5A-C



NAME=GA	YPD	GA	PGA	GA/YPD	PGA/YPD
ORF YIL101C	20	48	133	2.40	6.65
ORF YLR344W exon 1 (_i)	33	138	208	4.18	6.30
ORF YHR217C (_i)	20	29	120	1.45	6.00
ORF YHR217C (_f)	20	26	120	1.30	6.00
ORF YPL080C	20	56	114	2.80	5.70
ORF YPR098C	37	43	203	1.16	5.49
ORF YHL040C	27	55	135	2.04	5.00
ORF YOL080C	23	31	109	1.35	4.74
PHO84 (YML123C)	33	46	155	1.39	4.70
ORF YMR293C	28	36	114	1.29	4.07
ORF YLR184W	66	88	214	1.33	3.24
ORF YIL011W	153	154	460	1.01	3.01
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94
CYT1 (YOR065W)	91	93	257	1.02	2.82
ORF YLL025W (_f)	251	355	693	1.41	2.76
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73
ATP11 (YNL315C)	51	66	135	1.29	2.65
ORF YOR091W	59	69	148	1.17	2.51
ORF YMR143W exon 1 (_i)	385	895	964	2.32	2.50
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46
SKO1 (YNL167C)	43	20	101	0.47	2.35
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12
ORF YNL006W	77	100	161	1.30	2.09
MSI4 (YOR370C)	63	46	130	0.73	2.06
ORF YPR139C	91	122	187	1.34	2.05
SPO15 (YKR001C)	35	141	59	4.03	1.69
HHO1 (YPL127C)	81	45	135	0.56	1.67
ILV3 (YJR016C)	119	72	182	0.61	1.53
ORF YBR105C	82	20	120	0.24	1.46
LYS4 (YDR234W)	479	244	576	0.51	1.20
ORF YOR009W	144	310	158	2.15	1.10
NDC1 (YML031W)	113	33	115	0.29	1.02
ORF YOL073C	143	180	88	1.26	0.62
ORF YJL223C (_f)	134	175	81	1.31	0.60
ORF YMR242C	1170	1227	610	1.05	0.52
ORF YOR248W (_f)	497	422	239	0.85	0.48
ORF YPL081W exon 1	159	135	75	0.85	0.47
ORF YML019W	177	91	82	0.51	0.46
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46
ORF YMR050C exon 1 (_f)	374	263	169	0.70	0.45
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39
ORF YNR035C	200	249	78	1.25	0.39
ORF YEL033W	172	20	66	0.12	0.38
TSL1 (YML100W)	103	20	39	0.19	0.38
RPS33A (YOR167C) (_f)	1726	1899	589	1.10	0.34
ORF YFL032W	122	98	37	0.80	0.30
ORF YIL176C (_f)	115	99	34	0.86	0.30
COQ2 (YNR041C)	84	115	21	1.37	0.25
ORF YDL173W	141	136	34	0.96	0.24
ORF YOL002C	111	151	20	1.36	0.18
ORF YDL145C	118	74	20	0.63	0.17
PROCESS=scaling	METHOD=bulk SOURCE=GA.scl				
PROCESS=assemble.pl	GENES=6365 SOURCE=				
PROCESS=filter	GENES=53	DIFF=80	MAX=	RAT=2	

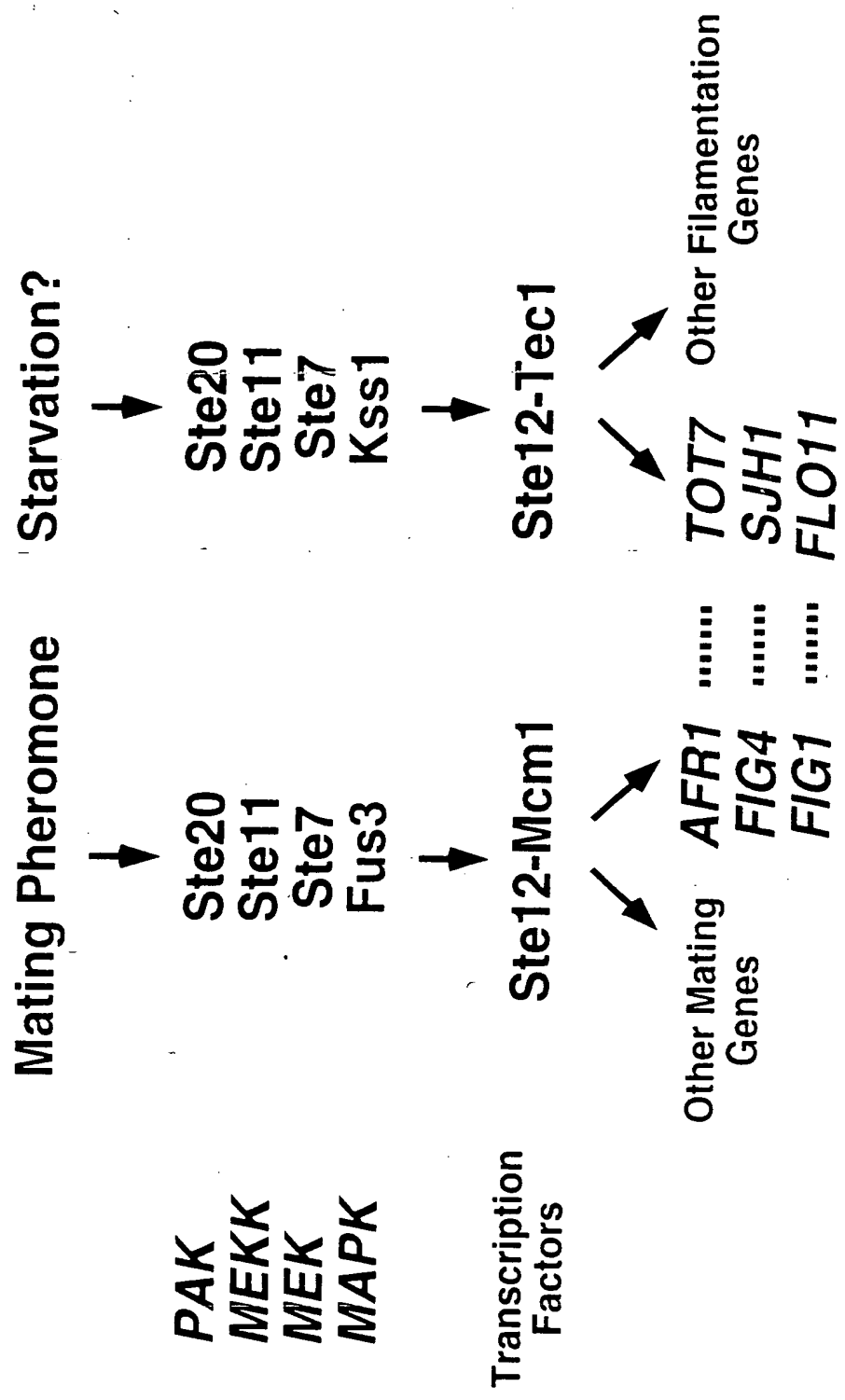


GA.filt.GAsort

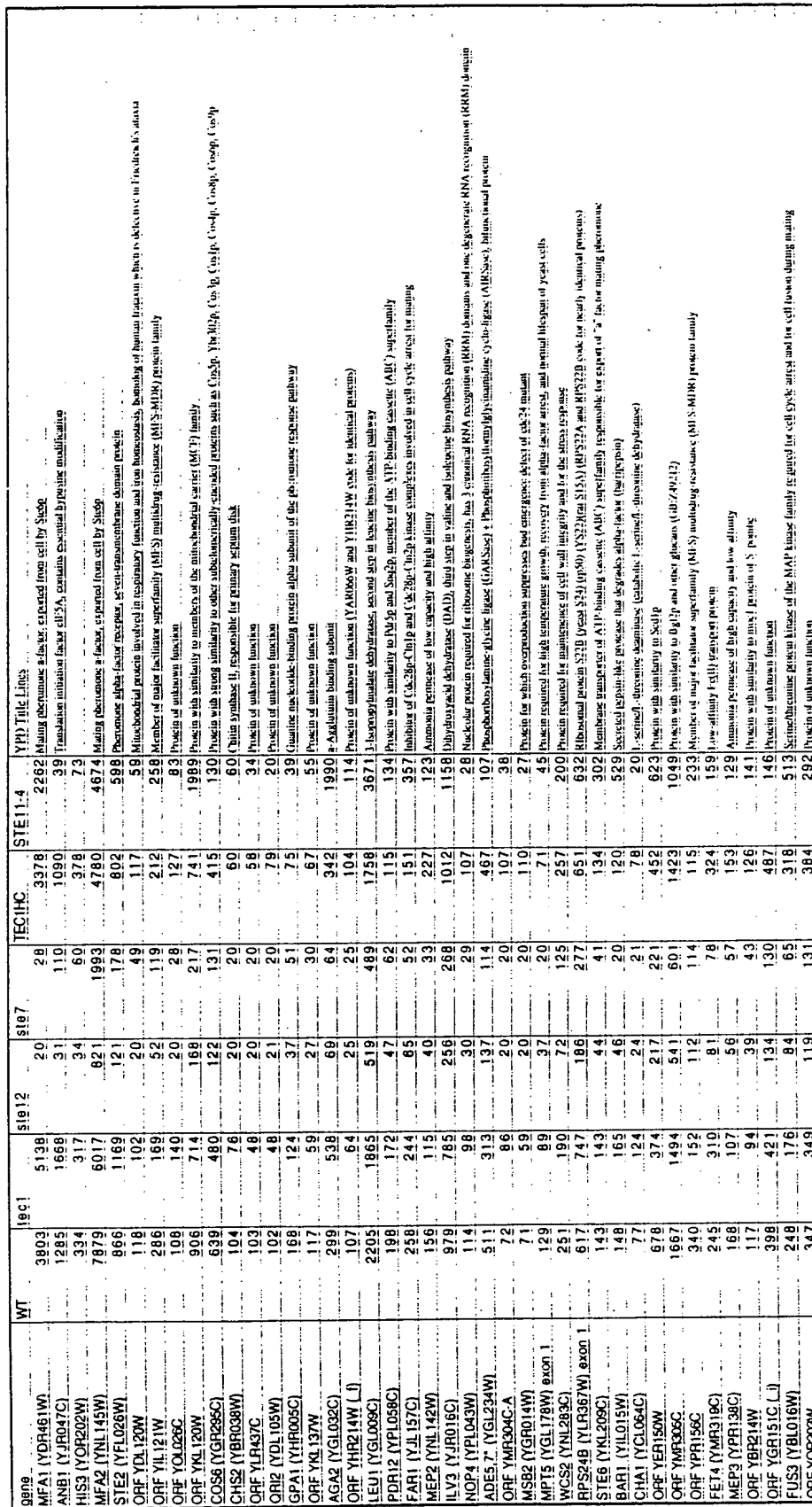
NAME-GA	YFD	GA	PGA	GA/YPD	PGA/YPD
ORF YLR344W exon 1 (_i)	33	138	208	4.18	6.30
SPO15 (YKR001C)	35	141	59	4.03	1.69
ORF YPL080C	20	56	114	2.80	5.70
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73
ORF YIL101C	20	48	133	2.40	6.65
ORF YMR143W exon 1 (_i)	385	895	964	2.32	2.50
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94
ORF YOR009W	144	310	158	2.15	1.10
ORF YHL040C	27	55	135	2.04	5.00
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15
ORF YHR217C (_r_i)	20	29	120	1.45	6.00
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12
ORF YLL025W (_f)	251	355	693	1.41	2.76
PHO84 (YML123C)	33	46	155	1.39	4.70
COQ2 (YNR041C)	84	115	21	1.37	0.25
ORF YOL002C	111	151	20	1.36	0.18
ORF YOL080C	23	31	109	1.35	4.74
ORF YPR139C	91	122	187	1.34	2.05
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46
ORF YLR184W	66	88	214	1.33	3.24
ORF YJL223C (_f)	134	175	81	1.31	0.60
ORF YHR217C (_f)	20	26	120	1.30	6.00
ORF YNL006W	77	100	161	1.30	2.09
ATP11 (YNL315C)	51	66	135	1.29	2.65
ORF YMR293C	28	36	114	1.29	4.07
ORF YOL073C	143	180	88	1.26	0.62
ORF YNR035C	200	249	78	1.25	0.39
ORF YOR091W	59	69	148	1.17	2.51
ORF YPR098C	37	43	203	1.16	5.49
RPS33A (YOR167C) (_f)	1726	1899	589	1.10	0.34
ORF YMR242C	1170	1227	610	1.05	0.52
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46
CYT1 (YOR065W)	91	93	257	1.02	2.82
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46
ORF YIL011W	153	154	460	1.01	3.01
ORF YDL173W	141	136	34	0.96	0.24
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39
ORF YIL176C (_f)	115	99	34	0.86	0.30
ORF YOR248W (_f)	497	422	239	0.85	0.48
ORF YPL081W exon 1	159	135	75	0.85	0.47
ORF YFL032W	122	98	37	0.80	0.30
MSI4 (YOR370C)	63	46	130	0.73	2.06
ORF YMR050C exon 1 (_f)	374	263	169	0.70	0.45
ORF YDL145C	118	74	20	0.63	0.17
ILV3 (YJR016C)	119	72	182	0.61	1.53
HHO1 (YPL127C)	81	45	135	0.56	1.67
ORF YML019W	177	91	82	0.51	0.46
LYS4 (YDR234W)	479	244	576	0.51	1.20
SKO1 (YNL167C)	43	20	101	0.47	2.35
NDC1 (YML031W)	113	33	115	0.29	1.02
ORF YBR105C	82	20	120	0.24	1.46
TSL1 (YML100W)	103	20	39	0.19	0.38
ORF YEL033W	172	20	66	0.12	0.38
PROCESS=scaling METHOD=bulk SOURCE=GA.scl					
PROCESS=assemble.pl GENES=6365 SOURCE=					
PROCESS=filter GENES=53 DIFF=80 MAX= RAT=2					
=					

~~Figure 9~~ Figure 7

Homologous Genes Induced by Filamentation and Mating MAPK Pathways



~~Figure 10~~ Figure 8



~~Figure 11~~ Figures 9A-B



MAPK Targets Include Proteins Known or Predicted to Enter the Secretory Pathway

PGU1	secreted endopolygalacturonase
FLO11	GPI-linked cell surface adhesion factor
TOT10/YEL033W	novel
SRD1	Zinc finger protein
TOT12/YKR105C	putative permease
TOT13/YOR225W	putative membrane protein
FLO5	GPI-linked cell surface adhesion factor
DDR48	cell surface protein
TOT11/YLR042C	GPI-linked cell surface protein
TOT7/YER158C	Homolog of mating morphogenesis protein Afr1
TOT8/YIL117C	Homolog of Chitin Synthase III subunit
TOT20/YHL049C	telomeric protein family member
TOT15/YLR434C	novel
TOT14/YBR113W	putative membrane protein
TOT9/YIR013C	Zinc finger protein
PHO84	phosphate transporter, sugar permease family
KTR2	protein mannosyltransferase homolog
SJH1	Sac1-related inositol phosphate 5-phosphatase homolog

Figure 1



Sytematic Knockout Experiments

GENE	Haploid Invasion	Diploid Filamentation
<i>PGU1</i>	+++	+++
<i>FLO11</i>	-	-
<i>TOT10/YEL033W</i>	+	+
<i>SRD1</i>	ND	ND
<i>TOT12/YKR105C</i>	+++	+++
<i>TOT13/YOR225W</i>	+++	+++
<i>FLO5</i>	+++	+++
<i>DDR48</i>	+++	+++
<i>TOT11/YLR042C</i>	+++	+++
<i>TOT7/YER158C</i>	+++	+++
<i>TOT8/YIL117C</i>	+++	+++
<i>TOT20/YHL049C</i>	ND	ND
<i>TOT15YLR434C</i>	+++	+++
<i>TOT14/YBR113W</i>	+++	+++
<i>TOT9/YIR013C</i>	+++	+++
<i>PHO84</i>	+++	+++
<i>KTR2</i>	+++	+++
<i>SJH1</i>	+++	+++

Figure 2



Gene Induction by the Plant-Specific Carbohydrate Polygalacturonic Acid and Its Hydrolysis Product

Genes Selectively Induced by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>XBP1</i>	2.40	6.65	Stress-induced transcriptional repressor
<i>YHR217C</i> (f)	1.30	6.00	Protein of unknown function
<i>YPL080C</i>	2.80	5.70	Protein of unknown function
<i>YPR098C</i>	1.16	5.49	Protein of unknown function
<i>YHL040C</i>	2.04	5.00	Putative MFS Permease
<i>YOL080C</i>	1.35	4.74	Protein with similarity to Rnh70p and Pan2p
<i>PHO84</i>	1.39	4.70	phosphate transport, sugar permease homolog*
<i>YMR293C</i>	1.29	4.07	Protein with similarity to amidase
<i>YLR184W</i>	1.33	3.24	Protein of unknown function
<i>YIL011W</i>	1.01	3.01	Protein with similarity to PAU1 family
<i>CYT1</i>	1.02	2.82	Cytochrome c1
<i>ATP11</i>	1.29	2.65	F1-ATP synthase assembly protein
<i>YOR091W</i>	1.17	2.51	Protein of unknown function
<i>PAU3</i>	1.02	2.46	Stress-induced protein of the PAU1 family
<i>SKO1</i>	0.47	2.35	ATF/CREB transcriptional repressor
<i>MSI4</i>	0.73	2.06	Rab guanine nucleotide dissociation inhibitor

Regulated by Filamentation MAPK Pathway*

Genes Selectively Induced by Galacturonic Acid

gene	GA/-	PGA/-	Protein Information
<i>VPS1</i>	4.03	1.69	Vacuolar sorting protein, dynamin GTPase

Figure 3



Gene Repression by the Plant-Specific Carbohydrate Polygalacturonic Acid and its Hydrolysis Product

Genes Selectively Repressed by Polygalacturonic Acid

gene	GA/-	PGA/-	Protein Information
COP1/SEC33	0.63	0.17	alpha subunit of coater complex
YOL002C	1.36	0.18	Protein of unknown function
YDL173W	0.96	0.24	Protein of unknown function
COQ2	1.37	0.25	coenzyme Q (ubiquinone) biosynthesis
YIL176C (f)	0.86	0.30	Protein with similarity to PAU1 family
YFL032W	0.80	0.30	Protein of unknown function
RPS33A	1.10	0.34	Ribosomal protein S28A
ARC35	1.25	0.39	Component of ARP2/3 complex
RPS26A	0.87	0.39	Ribosomal protein S26A
RPS10A	1.02	0.46	Ribosomal protein S10A

Genes Selectively Repressed by Galacturonic Acid

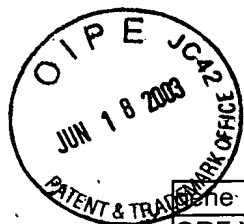
gene	GA/-	PGA/-	Protein Information
YEL033W	0.12	0.38	Protein of unknown function*
VID24	0.24	1.46	Vacuolar import and degradation of Fbp1
NDC1	0.29	1.02	Spindle pole body duplication factor
SKO1	0.47	2.35	ATF/CREB transcriptional repressor

*Regulated by the Filamentation MAPK Pathway



MAPK DATA							
floor = 20 max-min>90 scaling=bulk							
gene	WT	tec1	ste12	ste7	TEC1HC	STE11-4	YPD Title Line
STA1 (YIR019C)	262	47	45	173	742	2020	Cell surface flocculin
PGU1 (YJR153W)	50	20	34	21	269	28	Polygalacturonase, pectin-hydrolyzing enzyme
ORF YEL033W	178	20	41	30	256	20	Protein of unknown function
DDR48 (YMR173W-A)	492	147	147	148	1258	660	Stress protein induced by heat, shock, DNA damage, or osmotic stress
ORF YLR042C	91	33	20	20	275	968	Protein of unknown function
SRD1 (YCR018C)	57	20	20	20	150	65	Nucleolar protein involved in pre-rRNA processing does not bind to small nucleolar RNA (snoRNA)
ORF YAR009C (_f)	657	90	165	336	657	1250	Protein of unknown function
ORF YHR214C-B exon 1 (_f)	261	59	60	75	403	544	Protein of unknown function
ORF YKR105C	112	20	44	45	116	74	Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family
ORF YOR225W	66	20	47	45	109	164	Protein of unknown function
ORF YLR434C	105	21	51	29	113	76	Protein of unknown function
ORF YBR113W	75	30	48	138	159	257	Protein of unknown function
ORF YAR009C (_i)	672	134	364	665	655	2273	Protein of unknown function
ORF YIR013C	69	26	20	20	120	51	Protein of unknown function
PHO84 (YML123C)	79	25	78	26	114	77	High-affinity inorganic phosphate/H ⁺ symporter, member of sugar permease family
ORF YAR009C (_r_i)	724	160	348	620	702	2168	Protein of unknown function
KTR2 (YKR061W)	68	30	68	59	128	146	Mannosyltransferase of KRE2 family, involved in N-linked glycosylation
ORF YMR173W	20	33	20	20	136	91	Stress protein induced by heat shock, DNA damage, or osmotic stress
TEC1 (YBR083W)	612	332	45	62	1201	223	Transcriptional activator involved with STE12 in pseudohyphal formation
DAN1 (YJR150C)	170	29	20	108	104	20	Protein induced during anaerobic growth
SOR1 (YJR159W) (_f)	132	65	119	163	233	208	Sorbitol dehydrogenase, converts L-sorbitol and NAD to L-sorbose and NADH (SOR1 and YDL246C code for nearly identical proteins)
ORF YIL117C	20	20	20	20	69	195	Protein of unknown function
ORF YHR214C-B exon 2 (_f)	305	137	167	162	472	267	Protein of unknown function
ORF YNL256W	59	34	87	55	117	60	Protein with similarity to bacterial dihydropteroate synthase
GAP1 (YKR039W)	401	126	327	304	424	406	General amino acid permease, proton symport transporter for all naturally-occurring L-amino acids, 4-aminobutyric acid (GABA), ornithine, citrulline, some D-amino acids, and some toxic analogs
ORF YFL030W	20	26	38	47	87	175	Protein with similarity to Methanobacterium aspartate transaminase
ORF YLR152C	57	33	75	73	110	159	Protein with similarity to Ecm3p

Figure 5A



Gene	WT	tec1	ste12	ste7	TEC1HC	STE11-4	YPD Title Line
ORF YGL088W	97	35	20	27	113	20	Protein with similarity to Cyanophora paradoxa ribosomal protein secY
GPM2 (YDL021W)	68	20	74	69	63	131	Phosphoglycerate mutase, with similarity to Gpm1p and Gpm3p
ORF YFR024C-A exon 1	48	20	105	101	63	20	Protein with similarity to Ysc84p, Rvs167p, Abp1p, and Sla1p
PPG1 (YNR032W)	44	41	42	54	127	89	Protein serine/threonine phosphatase involved in glycogen accumulation, member of the PPP family of protein phosphatases and related to PP2A phosphatases
GCY1 (YOR120W)	45	27	89	54	78	180	Galactose-induced protein with strong similarity to crystallin protein of vertebrate eye lens
RHK1 (YBL082C)	153	57	133	121	164	136	Mannosyltransferase involved in N-glycosylation, Hansenula mrakii HM-1 killer toxin resistance protein
ORF YHL049C (_f)	20	20	20	20	57	107	Protein with similarity to other subtelomerically-encoded proteins including Yer189p, Ym1133p, and Yj1225p, coded from a subtelomeric Y' region
MUP3 (YHL036W)	54	31	146	70	86	56	Low affinity methionine amino acid permease
MUP1 (YGR055W)	179	94	315	280	257	192	High-affinity methionine permease
ORF YJR025C	1042	655	697	731	1731	1531	3-hydroxyanthranilate 3, 4-dioxygenase, involved in biosynthesis of nicotinic acid from tryptophan
ORF YDR111C	153	44	54	40	116	23	Protein with similarity to alanine aminotransferase (GB:Z48758)
TCI1 (YDR161W)	104	39	137	133	96	87	Protein that interacts with protein phosphatase 2C
PDE2 (YOR360C)	102	61	118	96	149	110	3', 5' -Cyclic-nucleotide phosphodiesterase
CWP1 (YKL096W)	149	76	176	186	181	430	Mannoprotein of the cell wall, member of the PAU1 family
ORF YOL164W	67	39	90	121	92	81	Protein with similarity to Pseudomonas sp. alkyl sulfatase
ORF YAR066W (_f)	98	86	36	49	202	101	Protein of unknown function (YAR066W and YHR214W code for identical proteins)
AIP2 (YDL178W)	209	87	217	135	197	128	Actin interacting protein and homolog of D-lactate dehydrogenase Dldp
ORF YGR257C	87	42	176	120	95	103	Protein with similarity to members of the mitochondrial carrier family (MCF)
RFC3 (YNL290W)	47	47	20	20	105	20	Replication factor C, 40 kDa subunit, member of the DEAD box family
ORF YER049W	255	106	176	125	236	105	Protein of unknown function
TIP1 (YBR067C)	2232	1574	159	182	3483	2891	Cold- and heat - shock induced mannoprotein of the cell wall, member of the PAU1 family
ORF YLR231C	178	76	144	152	168	445	Protein with weak similarity to rat kynureninase (PIR:PS0370), likely active in tryptophan degradation and nicotinic acid synthesis

Figure 5B



App No.: 09/439,969
 Title: Targets of the Map Kinase Pathway in the
 Developmental Switch in Yeast
 Inventors: Hiten D. Madhani and Eric S. Lander

gene	WT	tec1	ste12	ste7	TEC1HC	STE11-4	YPD Title Line
PCL1 (YNL289W)	53	39	59	59	84	185	G1/S-specific cyclin that can interact with the Cdc28p-like kinase Pho85p
ARG1 (YOL058W)	779	460	1418	1405	971	1999	Argininosuccinate synthetase (citrulline-aspartate ligase)
ORF YOR248W (_f)	887	842	717	632	1775	943	Protein of unknown function
FTR1 (YER145C)	239	200	429	230	415	383	Iron permease that mediates high-affinity iron uptake
ORF YNR018W	1947	1008	2056	1789	2089	2619	Protein of unknown function
CIT2 (YCR005C)	1555	820	1815	1324	1697	1682	Citrate synthase, peroxisomal, converts citrate plus CoA into acetyl-CoA and oxaloacetate
ORF YOR292C	49	66	59	47	135	86	Protein of unknown function
ORF YEL006W	105	63	119	85	127	43	Protein with similarity to Aac1p, Pet9p, Aac3p, Yi1006p and other members of the mitochondrial carrier (MCF) family
SVS1 (YPL163C)	650	426	337	274	858	1692	Serine- and threonine-rich protein required for vanadate resistance
ELO1 (YJL196C)	765	607	670	695	1218	1022	Fatty acid elongation protein involved in elongation of tetradecanoic acid to hexadecanoic acid
ORF YJL145W	165	174	253	148	349	337	Protein of unknown function
ORF YHR108W	60	20	114	91	40	112	Protein of unknown function
VID24 (YBR105C)	127	63	85	115	126	400	Protein required for vacuolar import and degradation of Fbp1p (Hui-Lin Chiang, pers. comm.)
ORF YOR389W	67	38	77	122	76	80	Protein of unknown function
LSC2 (YGR244C)	75	45	148	109	90	260	Beta subunit of succinyl-CoA synthetase (succinyl-CoA ligase) (succinate thiokinase)
CLP1 (YOR250C)	63	41	124	131	82	142	Subunit of cleavage and polyadenylation factor IA required for 3'-end processing of pre-mRNA

Figure 5C



NAME = GA					
gene	YPD	GA	PGA	GA/YPD	PGA/YPD
ORF YIL101C	20	48	133	2.4	6.65
ORF YLR344W exon 1 (_i)	33	138	208	4.18	6.3
ORF YHR217C (_r_i)	20	29	120	1.45	6
ORF YHR217C (_f)	20	26	120	1.3	6
ORF YPL080C	20	56	114	2.8	5.7
ORF YPR098C	37	43	203	1.16	5.49
ORF YHL040C	27	55	135	2.04	5
ORF YOL080C	23	31	109	1.35	4.74
PHO84 (YML123C)	33	46	155	1.39	4.7
ORF YMR293C	28	36	114	1.29	4.07
ORF YLR184W	66	88	214	1.33	3.24
ORF YIL011W	153	154	460	1.01	3.01
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94
CYT1 (YOR065W)	91	93	257	1.02	2.82
ORF YLL025W (_f)	251	355	693	1.41	2.76
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73
ATP11 (YNL315C)	51	66	135	1.29	2.65
ORF YOR091W	59	69	148	1.17	2.51
ORF YMR143W exon 1 (_i)	385	895	964	2.32	2.5
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46
SKO1 (YNL167C)	43	20	101	0.47	2.35
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12
ORF YNL006W	77	100	161	1.3	2.09
MS14 (YOR370C)	63	46	130	0.73	2.06
ORF YPR139C	91	122	187	1.34	2.05
SPO15 (YKR001C)	35	141	59	4.03	1.69
HHO1 (YPL127C)	81	45	135	0.56	1.67
ILV3 (YJR016C)	119	72	182	0.61	1.53
ORF YBR105C	82	20	120	0.24	1.46
LYS4 (YDR234W)	479	244	579	0.51	1.2
ORF YOR009W	144	310	158	2.15	1.1
NDC1 (YML031W)	113	33	115	0.29	1.02
ORF YOL073C	143	180	88	1.26	0.62
ORF YJL223C (_f)	134	175	81	1.31	0.6
ORF YMR242C	1170	1227	610	1.05	0.52
ORF YOR248W (_f)	497	422	239	0.85	0.48
ORF YPLL081W exon 1	159	135	75	0.85	0.47
ORF YML019W	177	91	82	0.51	0.46
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46
ORF YMR050C exon 1 (_f)	374	263	169	0.7	0.45
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39
ORF YNR035C	200	249	78	1.25	0.39
ORF YEL033W	172	20	66	0.12	0.38
TSL1 (YML100W)	103	20	39	0.19	0.38
RPS33A (YOR167C) (_f)	1726	1899	589	1.1	0.34
ORF YFL032W	122	98	37	0.8	0.3
ORF YIL176C (_f)	115	99	34	0.86	0.3
COQ2 (YNR041C)	84	115	21	1.37	0.25
ORF YDL173W	141	136	34	0.96	0.24
ORF YOL002C	111	151	20	1.36	0.18
ORF YDL145C	118	74	20	0.63	0.17
PROCESS=scaling	METHOD=bulk	SOURCE=GA.sci			
PROCESS=assemble.pl	GENES=6365	SOURCE=GA.sci			
PROCESS=filter	GENES=53	DIFF=80	MAX=	RAT=	

Figure 6



GA.filt.GAsort					
NAME=GA					
gene	YPD	GA	PGA	GA/YPD	PGA/YPD
ORF YLR344W exon 1 (_l)	33	138	208	4.18	6.30
SPO15 (YKR01C)	35	141	59	4.03	1.69
ORF YPL080C	20	56	114	2.80	5.70
ORF YML039W exon 2 (_f)	192	486	524	2.53	2.73
ORF YIL101C	20	48	133	2.40	6.65
ORF YMR143W exon 1 (_l)	385	895	964	2.32	2.50
ORF YJR027W exon 2 (_f)	156	351	459	2.25	2.94
ORF YOR009W	144	310	158	2.15	1.10
ORF YHL040C	27	55	135	2.04	5.00
PRE3 (YJL001W) exon 1	112	166	241	1.48	2.15
ORF YHR217C (_r_l)	20	29	120	1.45	6.00
ORF YMR045C exon 2 (_f)	93	132	197	1.42	2.12
ORF YLL025W (_f)	251	355	693	1.41	2.76
PHO84 (YML123C)	33	46	155	1.39	4.70
COQ2 (YNR041C)	84	115	21	1.37	0.25
ORF YOL002C	111	151	20	1.36	0.18
ORF YOL080C	23	31	109	1.35	4.74
ORF YPR139C	91	122	187	1.34	2.05
ORF YJR029W exon 2 (_f)	71	95	175	1.34	2.46
ORF YLR184W	66	88	214	1.33	3.24
ORF YJL223C (_f)	134	175	81	1.31	0.60
ORF YHR217C (_f)	20	26	120	1.30	6.00
ORF YNL006W	77	100	161	1.30	2.09
ATP11 (YNL315C)	51	66	135	1.29	2.65
ORF YMR293C	28	36	114	1.29	4.07
ORFYOL073C	143	180	88	1.26	0.62
ORF YNR035C	200	249	78	1.25	0.39
ORF YOR091W	59	69	148	1.17	2.51
ORF YPR098C	37	43	203	1.16	5.49
RPS33A (YOR167C) (_f)	1726	1899	589	1.10	0.34
ORF YMR242C	1170	1227	610	1.05	0.52
PAU3 (YCR104W) (_f)	180	184	443	1.02	2.46
CYT1 (YOR065W)	91	93	257	1.02	2.82
ORF YOR293W exon 1 (_f)	3170	3237	1446	1.02	0.46
ORF YIL011W	153	154	460	1.01	3.01
ORF YDL173W	141	136	34	0.96	0.24
RPS26A (YGL189C)	11511	9978	4526	0.87	0.39
ORF YIL176C (_f)	115	99	34	0.86	0.30
ORF YOR248W (_f)	497	422	239	0.85	0.48
ORF YPL081W exon 1	159	135	75	0.85	0.47
ORF YFL032W	122	98	37	0.80	0.30
MS14 (YOR370C)	63	46	130	0.73	2.06
ORF YMR050C exon 1 (_f)	374	263	169	0.70	0.45
ORF YDL145C	118	74	20	0.63	0.17
ILV3 (YJR016C)	119	72	182	0.61	1.53
HHO1 (YPL127C)	81	45	135	0.56	1.67
ORF YML019W	177	91	82	0.51	0.46
LYS4 (YDR234W)	479	244	576	0.51	1.20
SKO1 (YNL167C)	43	20	101	0.47	2.35
NDC1 (YML031W)	113	33	115	0.29	1.02
ORF YBR105C	82	20	120	0.24	1.46
TSL1 (YML100W)	103	20	39	0.19	0.38
ORF YEL033W	172	20	66	0.12	0.38
PROCESS=scaling	METHOD=bulk	SOURCE=GA.sci			
PROCESS=assemble.pi	GENES=6365	SOURCE=			
PROCESS=filter	GENES=53	DIFF=80	MAX=	RAT=2	

Figure 7



Homologous Genes Induced by Filamentation and Mating MAPK Pathways

App No.: 09/439,969
Title: Targets of the Map Kinase Pathway in the
Developmental Switch in Yeast
Inventors: Hiten D. Madhani and Eric S. Lander

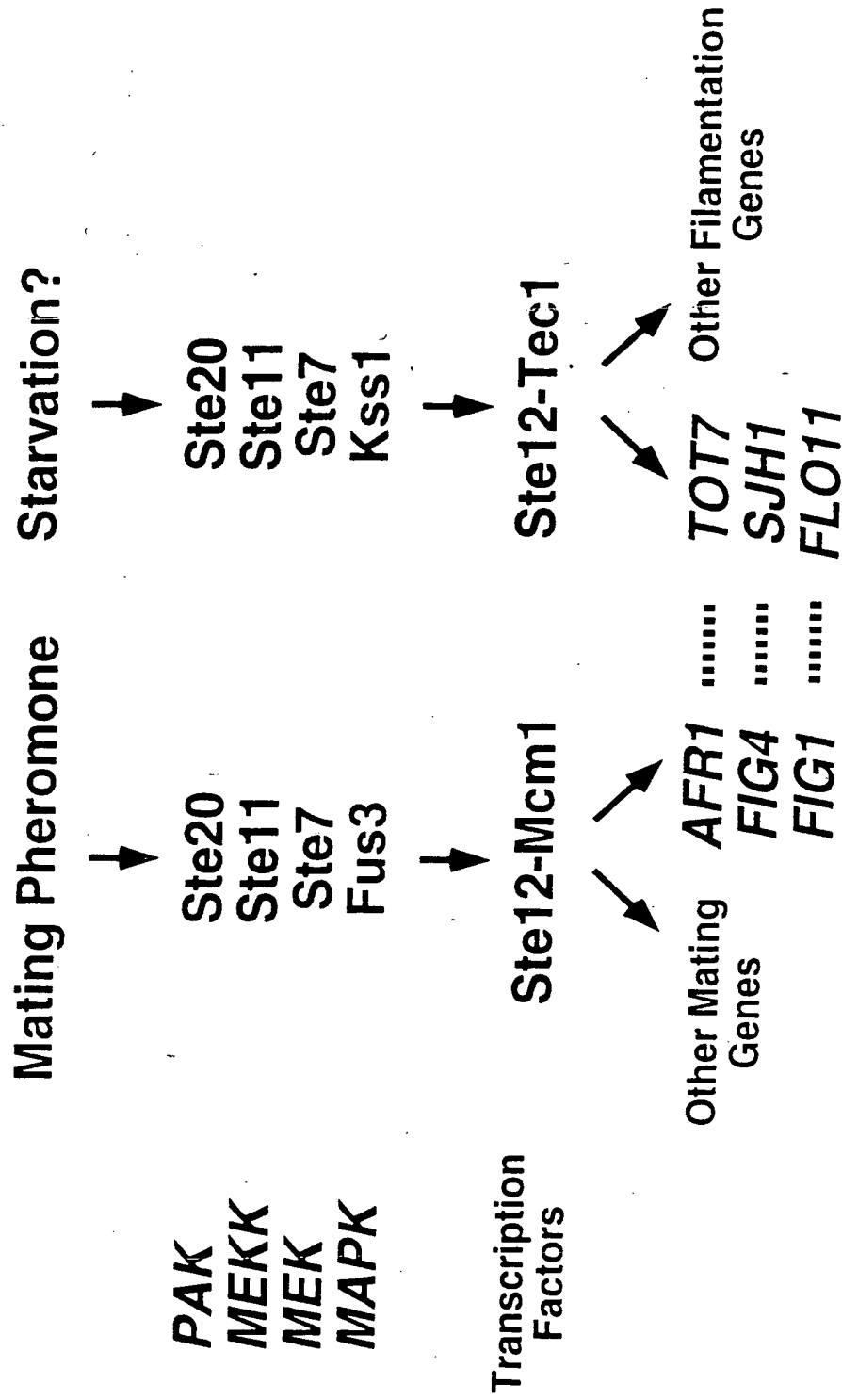


Figure 8



App No.: 09/439,969

Title: Targets of the Map Kinase Pathway in the Developmental Switch in Yeast

Inventors: Hiten D. Madhani and Eric S. Lander

Gene	WT	tec1	ste12	ste7	TEC1HC	STE11-4	YPD Title Lines
MFA1 (YDR461W)	380 3	5138	20	28	3378	2262	Mating pheromone a-factor, exported from cell by ste6p
ANB1 (YJR047C)	128 5	1668	31	110	1090	39	Translation initiation factor eIF5A, contains essential bypsine modification
HIS3 (YOR202W)	334	317	34	60	378	73	
MFA2 (YNL145W)	787 9	6017	821	1993	4780	4674	Mating pheromone a-factor, exported from cell by Ste6p
STE2 (YFL026W)	866	1169	121	178	802	598	Pheromone alpha-factor receptor, seven-transmembrane domain protein
ORF YDL120W	118	102	20	49	117	59	Mitochondrial protein involved in respiratory function and iron homeostatis, homolog of human frataxin which is defective in Friedreich's ataxia
ORF YIL121W	286	169	52	119	212	258	Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family
ORF YOL026C	108	140	20	28	127	83	Protein of unknown function
ORF YKL120W	906	714	168	217	741	1989	Protein with similarity to members of the mitochondrial carrier (MCF) family
COS6 (YGR295C)	639	480	122	131	415	130	Protein with strong similarity to other subtelomerically-encoded proteins such as Cos5p, Ybr302p, Cos3p, Cos1p, Cos4p, Cos8p, Cos6p, Cos9p
CHS2 (YBR038W)	104	76	20	20	60	60	Chitin synthase II, responsible for primary septum disk
ORF YLR437C	103	48	20	20	58	34	Protein of unknown function
QR12 (YDL105W)	102	48	21	20	79	20	Protein of unknown function
GPA1 (YHR005C)	168	124	37	51	75	39	Guanine nucleotide-binding protein alpha subunit of the pheromone response pathway
ORF YKL137W	117	59	27	30	67	55	Protein of unknown function
AGA2 (YGL032C)	299	538	69	64	342	1990	a-Agglutinin binding subunit
ORF YHR214W (_f)	107	64	25	25	104	114	Protein of unknown function (YAR066W and YHR214W code fo identical proteins)
LEU1 (YGL009C)	220 5	1865	519	489	1758	3671	3-Isopropylmalate dehydratase, second step in leucine biosynthesis pathway
PDR12 (YPL058C)	198	172	47	62	115	134	Protein with similarity to Pdr5p and Snq2p, member of the ATP-binding cassette (ABC) superfamily
FAR1 (YJL157C)	258	244	65	52	151	357	Inhibitor of Cdc28p-Cln1p and Cdc28p-Cln2p kinase complexes involved in cell cycle arrest for mating
MEP2 (YNL142W)	156	115	40	33	227	123	Ammonia permease of low capacity and high affinity
ILV3 (YJR016C)	979	785	256	268	1012	1158	Dihydroxyacid dehydratase (DAD), third step in valine and isoleucine biosynthesis pathway
NOP4 (YPL043W)	114	98	30	29	107	28	Nucleolar protein required for ribosome biogenesis, has 3 canonical RNA recognition (RRM) domains and one degenerate RNA recognition (RRM) domain

Figure 9A



Gene	WT	tec1	ste12	ste7	TEC1HC	STE11-4	YPD Title Lines
ADE5,7" (YGL234W)	511	313	137	114	467	107	Phosphoribosylamine-glycine ligase (GARSase) + Phosphoribosylformylglycinamide cyclo-ligase (AIRSase), bifunctional protein
ORF YMR304C-A	72	86	20	20	107	38	
MSB2 (YGR014W)	71	59	20	20	110	27	Protein for which overproduction suppresses bud emergence defect of cdc24 mutant
MPT5 (ygL178w) exon 1	129	89	37	20	71	45	Protein required for high temperature growth, recovery from alpha-factor arrest, and normal lifespan of yeast cells
WCS2 (YNL283C)	251	190	72	125	257	200	Protein required for maintenance of cell wall integrity and for the stress response
RPS24B (YLR367W) exon 1	617	747	186	277	651	632	Ribosomal protein S22B (yeast S24) (rp50) (YS22)(ratS15A) (RPS22A and RPS22B code for nearly identical proteins)
STE6 (YKL209C)	143	143	44	41	134	302	Membrane transporter of ATP-binding cassette (ABC) superfamily responsible for export of "a" factor mating pheromone
BAR1 (YIL015W)	148	165	46	20	120	529	Secreted pepsin-like protease that degrades alpha-factor (barripepsin)
CHA1 (YCL064C)	77	124	24	21	78	20	L-serine/L-threonine deaminase (catabolic L-serine/L-threonine dehydratase)
ORF YER150W	678	374	217	221	452	623	Protein with similarity to Sed1p
ORF YMR305C	166 7	1494	541	601	1423	1049	Protein with similarity to Bg12p and other glucans (GB:Z49212)
ORF YPR156C	340	152	112	114	115	233	Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family
FET4 (YMR319C)	245	310	81	78	324	159	Low-affinity Fe(II) transport protein
MEP3 (YPR138C)	168	107	56	57	153	129	Ammonia permease of high capacity and low affinity
ORF YBR214W	117	94	39	43	126	141	Protein with similarity to moc1 protein of S. pombe
ORF YGR151C (_i)	398	421	134	130	487	146	Protein of unknown function
FUS3 (YBL016W)	248	176	84	65	318	513	Serine/threonine protein kinase of the MAP kinase family required for cell cycle arrest and for cell fusion during mating
ORF YOR203W	347	349	119	131	384	292	Protein of unknown function

Figure 9B